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- 5) Richardson et al., Biol. Reprod., 62(3):789-796 (March 2000).
- 6) Baker et al., Nat. Genet., 13(3):336-342 (July 1996).
- 7) Hassold, Nat. Genet., 13(3):261-262 (July 1996).
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- 9) Hunter and Borts, Genes Dev., 11(12):1573-1582 (Jun. 15, 1997).
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Thanks in advance,

Peter Brunovskis
Art Unit 1632
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Mismatch repair goes meiotic

Terry J. Hassold

Department of Genetics,
Case Western Reserve University
and The Center for Human Genetics,
University Hospitals of Cleveland,
Cleveland, Ohio 44106, USA

Until recently, geneticists studying mammalian meiosis have experienced what might best be described as 'system envy'. While studies of yeast and *Drosophila* have yielded remarkable advances in understanding how homologous recombination and meiotic chromosome pairing, synapsis and segregation occur in these organisms¹, the pace has been much slower for mammals. However, as exemplified by the paper by Baker *et al.*² on page 336 in this issue, the situation is beginning to change. The identification of mammalian homologues of non-mammalian meiotic genes, and the subsequent generation of mouse knockouts for these genes, now make it possible to study the effects of specific mutations on the meiotic process.

Baker *et al.*² have used this approach to study one of the murine DNA mismatch repair genes, *Mlh1*. At first glance, this might seem an unlikely target. The mouse *Mlh1* protein is homologous to Mut1, one of the components of the MutHLS mismatch repair system of *E. coli*³. This is a complex system, requiring products from several genes, but three genes are key: *mutS* (encoding a DNA mismatch-binding protein), *mutH* (encoding a synthesized-strand binding protein) and *mutL* (encoding a protein that appears to promote MutS–MutH interactions and to enhance MutH activity). As the primary role of this system is the repair of replication errors it is not surprising that several of its components have been conserved through evolution; thus, genes encoding homologues to *MutL* and *MutS* have been identified in mammals as well as yeast.

In humans, mismatch repair mutants recently have attracted considerable attention due to their association with malignancy⁴. Mutations in either *MSH2* (homologous to *mutS*) or in *PMS1*, *PMS2* or *MLH1* (homologues to *mutL*) occur in families segregating hereditary non-polyposis colon cancer, one of the common cancer predisposition syndromes. Similarly,

mice engineered to carry mutations at mismatch repair loci have an increased susceptibility to tumour formation⁵.

However, in addition to its role in somatic tissues, mismatch repair fulfills an important function in the germ cell during meiotic prophase. A central feature of meiosis I is homologous recombination, an important component of which is the recognition and repair of mismatches in the heteroduplex DNA. Abnormalities in the repair system can have catastrophic meiotic consequences, as evidenced by studies in *Saccharomyces cerevisiae*. Mutations in the mismatch repair gene homologues *MSH2*, *MSH4*, *MSH5* and *PMS1* have been linked to a variety of meiotic abnormalities, including aberrant recombination, post-meiotic segregation and nondisjunction⁶.

Baker *et al.*² demonstrate that mutations in mammalian mismatch repair also disrupt the meiotic process. They used homologous recombination to target the murine *Mlh1* locus in embryonic stem cells and subsequently generated animals heterozygous and homozygous for mutation. The somatic effects were as expected: *Mlh1*–/– animals exhibit microsatellite instability and are likely predisposed to cancer, since a lymphoma was identified in a female sacrificed for ovarian studies.

The meiotic consequences are profound. Histological examination of testes for *Mlh1*–/– males demonstrate the presence of primary spermatocytes, but a complete absence of later stage cells, consistent with an arrest at meiosis I. Ovaries from *Mlh1*–/– females contain only a few follicles but corpora lutea are occasionally identified, indicating that ovulation can occur. However, breeding with *Mlh1*–/– females was unsuccessful and, as the males have no sperm, infertility is apparently a feature of both sexes.

What is the basis for these effects? To address this question, Baker *et al.*² took two approaches. First, they examined chromosome behaviour in meiosis I of *Mlh1*–/– spermato-

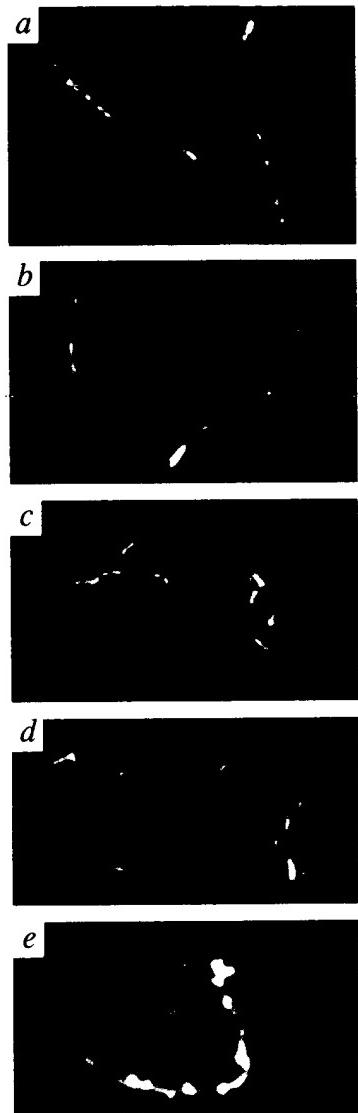


Fig. 1 Localization of *Mlh1* during meiosis. White = anti-Rad51; red = anti-*Mlh1*. a, Pachytene oocyte: *Mlh1* is seen as discrete foci along the paired axes of the synaptonemal complex. b, Early diplotene oocyte: As homologues begin to separate, *Mlh1* is located at junctures between synapsed and desynapsed axes, as well as at sites along the still synapsed axes. c, Diplotene oocyte: *Mlh1* is still visible at chiasmata sites. d, Late diplotene oocyte: *Mlh1* has disappeared from the chiasmata sites. e, XY chromosomes in early pachytene spermatocyte: a single *Mlh1* focus is found at the base of the XY-pairing site.

cytes. Initial pairing behaviour appears normal. However, by diplotene — when homologous chromosomes are normally still joined at the points of genetic exchange (the chiasmata) but are no

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Table 1 Effects of mismatch repair mutations on murine meiosis

| Protein (ref.) | <i>E. coli</i> homologue | Effect on male meiosis | Effect on female meiosis |
|-------------------|--------------------------|--|--|
| <i>Mlh1</i> (2) | <i>MutL</i> | Reduced numbers of chiasmata, premature separation of bivalents; males infertile | Reduced numbers of chiasmata, premature separation of bivalents; females infertile |
| <i>Pms2</i> (7) | <i>MutL</i> | synaptic abnormalities; males infertile | not tested; females fertile |
| <i>Msh2</i> (5,7) | <i>MutS</i> | Meiotic studies not conducted; mice fertile | |

longer fully synapsed — the homologous chromosomes in *Mlh1*-deficient spermatocytes are frequently separated from one another. That is, they are univalents. By metaphase of meiosis I, most of the chromosomes are in this configuration. This suggests that *Mlh1* promotes chiasma formation or stabilization and, consistent with this interpretation, analyses of diplotene and metaphase figures indicated a 10–100-fold reduction in chiasma frequency in *Mlh1*—/— spermatocytes.

Second, Baker *et al.*² used an antibody against *Mlh1* to examine its meiosis I localization in deficient males, and in normal males and females (Fig. 1). In oocytes of normal females, discrete *Mlh1* loci observed on synapsed portions of the synaptonemal complex (SC) as early as zygote. By early pachytene — at which time homologues are fully synapsed — several *Mlh1* loci per SC are seen (Fig. 1a); by mid-pachytene the number drops to about 1.5 foci per SC; and by early diplotene few foci are left but occasionally are observed at the sites of chiasmata (Fig. 1b–d).

In spermatocytes, *Mlh1* foci are not identified until early pachytene, but by mid-pachytene approximately 1.2 foci per SC are observed. Importantly, a focus is consistently identified at the distal end of the pairing region of the XY bivalent in early pachytene spermatocytes (Fig. 1e) but shortly thereafter — about the time when the X and Y begin to desynapse — no signal is observed.

These observations fulfill many of the predictions for a protein involved in chiasma processing: in *Mlh1*—/— spermatocytes, with a diminished number of chiasmata, there was no detectable *Mlh1*; in normal males and females, the total number of mid-pachytene foci corresponded to the expected number

of chiasmata and more foci were identified in oocytes than spermatocytes, consistent with the known difference in female to male recombination rates; and, in females, foci were occasionally observed at the sites of crossing-over. Taken together, these results provide compelling evidence that *Mlh1* fulfills an important function in meiosis I.

However, many important questions remain. For example, when does *Mlh1* act and what is its target? Based on the temporal expression pattern of *Mlh1*, Baker *et al.*² speculate that it may be a component of late recombination nodules, electron dense structures which correlate with crossing-over in many organisms¹. However, the nature and organization of mammalian recombination nodules remain obscure; thus, this association remains to be elucidated.

Also unclear are the meiosis I interactions, if any, between *Mlh1* and other mammalian mismatch repair proteins (see Table 1). In a previous study, Baker *et al.*⁷ analysed the consequences to murine spermatogenesis of a *Pms2* null mutation. *Pms2* and *Mlh1* are thought to interact with one another in somatic tissues, as they appear to be components of same repair pathway and form a heterodimer *in vitro*⁸. Thus, it is not surprising that *Pms2* mutations also disrupt spermatogenesis and that *Pms2*-deficient males are sterile⁷. However, what is somewhat surprising is the difference in phenotype between the two mutations: *Pms2* deficiency is evident earlier in meiosis I, associated with abnormalities in synapsis, and, unlike *Mlh1* deficiency, *Pms2*—/— mice produce some, although abnormal, spermatozoa. Further, *Pms2*-deficient females are fertile, indicating gender-specific differences in the meiotic roles of *Mlh1* and *Pms2*. Thus, it seems

unlikely that *Mlh1* and *Pms2* function coordinately in meiosis I; nor do they appear to interact with the MutS mammalian homologue *Msh2*. *Msh2*-deficient mice are fertile^{5,9}, providing little evidence for a meiotic role of this protein.

Finally, the clinical implications of these findings are yet to be determined. The consequences of meiotic abnormalities to human reproduction are enormous. For example, an estimated 5% of all clinically recognized human pregnancies (that is pregnancies surviving to at least 6–8 weeks gestation) and possibly as many as 20–25% of all human conceptuses are aneuploid as a result meiotic chromosome mis-segregation. Further, these values increase with age of the women, so that among women 40 years and older, it may be that a majority of oocytes are chromosomally abnormal. Despite this high incidence and obvious clinical importance, the basis of these abnormalities remains a complete mystery. Could it be that some proportion are due to meiotic mutations or to age-related degradation in *MLH1*, *PMS2* or in other meiotic proteins with which they interact? Further analyses of chromosome segregation, possibly using non-null mutations, will be extremely welcome.

Future studies notwithstanding, the present paper on *Mlh1* (ref. 2) and its predecessor on *Pms2* (ref. 7) are important milestones in mammalian meiotic analysis. This is not to say that mammalian geneticists do not still have ample reason to be envious of their colleagues studying meiosis in other organisms. They do. Yeast and *Drosophila* geneticists — with rough maps of the meiotic highway already in hand¹ — remain miles ahead of their mammalian counterparts. Nevertheless — at long last — mammalian geneticists can see the on-ramp. —

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